

## GENETIC DIVERSITY OF ISOLATED SUSCEPTIBLE TO FLUCONAZOL OF *Candida parapsilosis* COMPLEX

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### **Abstract:**

Among the species of non-*albicans* *Candida* involved in candidiasis there is the *Candida parapsilosis*, especially in hospitalized patients, where often this yeast is involved in bloodstream infections. However due to recent taxonomic changes of this species, it was necessary to separate *Candida parapsilosis* into three groups forming a complex, namely: *C. parapsilosis* named *sensu stricto* (corresponding to group I), *C. orthopsilosis* (group II) and *C. metapsilosis* (group III). Clinical isolates of this complex are generally sensitive to most antifungal agents; however, there can be found different patterns of susceptibility among the species, making the correct choice of antifungal drug used for the treatment a necessary task. In this context, this research assessed the genetic diversity among isolated of *C. parapsilosis* complex from diabetic and kidney transplanted patients and correlated with the level of susceptibility to fluconazole. For the molecular study, the amplification reaction of PCR fragments was used, followed by fragments sequencing of the region ITS1, 5.8S gene, ITS2 and fragments of the 28S rDNA gene. The technique of E-Test® was used in order to determine the minimum inhibitory concentration (MIC) of fluconazole. A consistent separation between the three species that comprise complex *C. parapsilosis* (*C. parapsilosis*, *C. metapsilosis* and *C. orthopsilosis*) with low intraspecific variability was observed in the analysis of genetic diversity. Although all isolated are sensitive to fluconazole, the MIC highest average was of *C. metapsilosis* (3.0 ug / ml).

**Keywords:** Genetic diversity, *Candida parapsilosis*, fluconazole.